

Input Set: I512363.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

1 <110> APPLICANT: Ni, Jian  
2 Ruben, Steven M.  
3 <120> TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins  
4 TR11, TR11SV1, and TR11SV2  
5 <130> FILE REFERENCE: PF396  
6 <140> CURRENT APPLICATION NUMBER: US/09/512,363  
7 <141> CURRENT FILING DATE: 2000-02-23  
8 <150> EARLIER APPLICATION NUMBER: 60/063,212  
9 <151> EARLIER FILING DATE: 1997-10-21  
10 <150> EARLIER APPLICATION NUMBER: 09/176,200  
11 <151> EARLIER FILING DATE: 1998-10-21  
12 <150> EARLIER APPLICATION NUMBER: 60/121,648  
13 <151> EARLIER FILING DATE: 1999-02-24  
14 <150> EARLIER APPLICATION NUMBER: 60/134,172  
15 <151> EARLIER FILING DATE: 1999-05-13  
16 <150> EARLIER APPLICATION NUMBER: 60/144,076  
17 <151> EARLIER FILING DATE: 1999-07-16  
18 <160> NUMBER OF SEQ ID NOS: 28  
19 <170> SOFTWARE: PatentIn Ver. 2.0  
20 <210> SEQ ID NO 1  
21 <211> LENGTH: 983  
22 <212> TYPE: DNA  
23 <213> ORGANISM: Homo sapiens  
24 <220> FEATURE:  
25 <221> NAME/KEY: CDS  
26 <222> LOCATION: (118)..(819)  
27 <220> FEATURE:  
28 <221> NAME/KEY: mat\_peptide  
29 <222> LOCATION: (193)..(819)  
30 <220> FEATURE:  
31 <221> NAME/KEY: scrna  
32 <222> LOCATION: (118)..(192)  
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34 gcacttcacc tgggtcggga ttctcaggtc atgaacgggc ccagccacct ccgggcaggg 60  
35 cgggtgagga cggggacggg gcgtgtccaa ctggctgtgg gctcttgaaa cccgagc 117  
36 atg gca cag cac ggg gcg atg ggc gcg ttt cgg gcc ctg tgc ggc ctg 165  
37 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu  
38 -25 -20 -15 -10  
39 gcg ctg ctg tgc gcg ctc agc ctg ggt cag cgc ccc acc ggg ggt ccc 213  
40 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro  
41 -5 -1 1 5  
42 ggg tgc ggc cct ggg cgc ctc ctg ctt ggg acg gga acg gac gcg cgc 261  
43 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg  
44 10 15 20

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/512,363

DATE: 03/20/2000  
TIME: 15:41:40

Input Set: I512363.RAW

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45      tgc tgc cgg gtt cac acg acg cgc tgc tgc cgc gat tac ccg ggc gag      309
46      Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
47          25                      30                      35
48      gag tgc tgt tcc gag tgg gac tgc atg tgt gtc cag cct gaa ttc cac      357
49      Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
50          40                      45                      50                      55
51      tgc gga gac cct tgc tgc acg acc tgc cgg cac cac cct tgt ccc cca      405
52      Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
53          60                      65                      70
54      ggc cag ggg gta cag tcc cag ggg aaa ttc agt ttt ggc ttc cag tgt      453
55      Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
56          75                      80                      85
57      atc gac tgt gcc tcg ggg acc ttc tcc ggg ggc cac gaa ggc cac tgc      501
58      Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
59          90                      95                      100
60      aaa cct tgg aca gac tgc acc cag ttc ggg ttt ctc act gtg ttc cct      549
61      Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
62          105                      110                      115
63      ggg aac aag acc cac aac gct gtg tgc gtc cca ggg tcc ccg ccg gca      597
64      Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
65          120                      125                      130                      135
66      gag ccg ctt ggg tgg ctg acc gtc gtc ctc ctg gcc gtg gcc gcc tgc      645
67      Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
68          140                      145                      150
69      gtc ctc ctc ctg acc tcg gcc cag ctt gga ctg cac atc tgg cag ctg      693
70      Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
71          155                      160                      165
72      agg aag acc cag ctg ctg ctg gag gtg ccg ccg tcg acc gaa gac gcc      741
73      Arg Lys Thr Gln Leu Leu Leu Glu Val Pro Pro Ser Thr Glu Asp Ala
74          170                      175                      180
75      aga agc tgc cag ttc ccc gag gaa gag cgg ggc gag cga tcg gca gag      789
76      Arg Ser Cys Gln Phe Pro Glu Glu Glu Arg Gly Glu Arg Ser Ala Glu
77          185                      190                      195
78      gag aag ggg cgg ctg gga gac ctg tgg gtg tgagcctggc cgtcctccgg      839
79      Glu Lys Gly Arg Leu Gly Asp Leu Trp Val
80      200                      205
81      ggccaccgac cgcagccagc ccctccccag gagctcccca ggccgcaggg gctctgcgtt      899
82      ctgctctggg ccggggccctg ctcccctggc agcagaagtg ggtgcaggaa ggtggcagtg      959
83      accagcgcgc tggaccatgc agtt      983
84      <210> SEQ ID NO 2
85      <211> LENGTH: 234
86      <212> TYPE: PRT
87      <213> ORGANISM: Homo sapiens
88      <400> SEQUENCE: 2
89      Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
90      -25                      -20                      -15                      -10
91      Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
92          -5                      -1      1                      5
93      Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
94          10                      15                      20

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95      Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
96          25                      30                      35
97      Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
98          40                      45                      50                      55
99      Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
100          60                      65                      70
101     Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
102          75                      80                      85
103     Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
104          90                      95                      100
105     Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
106          105                     110                     115
107     Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
108          120                     125                     130                     135
109     Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
110          140                     145                     150
111     Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
112          155                     160                     165
113     Arg Lys Thr Gln Leu Leu Leu Glu Val Pro Pro Ser Thr Glu Asp Ala
114          170                     175                     180
115     Arg Ser Cys Gln Phe Pro Glu Glu Glu Arg Gly Glu Arg Ser Ala Glu
116          185                     190                     195
117     Glu Lys Gly Arg Leu Gly Asp Leu Trp Val
118          200                     205
119 <210> SEQ ID NO 3
120 <211> LENGTH: 1007
121 <212> TYPE: DNA
122 <213> ORGANISM: Homo sapiens
123 <220> FEATURE:
124 <221> NAME/KEY: CDS
125 <222> LOCATION: (121)..(843)
126 <400> SEQUENCE: 3
127     gtcgacccac gcgtccgggg ggccaccctt gggctctgca ggggcagctc ctggttgcac 60
128     atggagttag cacctgggca ggggcagctg tggggcgcaa agggggagta gccaggccac 120
129     atg gcc cca gga gaa aga gac agc tgg ata aac cca ggt cca gac tcc 168
130     Met Ala Pro Gly Glu Arg Asp Ser Trp Ile Asn Pro Gly Pro Asp Ser
131         1                      5                      10                      15
132     cag cca gga gcc ctc tgc tcc ctg gag cca act gtg ggt gga gaa cgg 216
133     Gln Pro Gly Ala Leu Cys Ser Leu Glu Pro Thr Val Gly Gly Glu Arg
134         20                      25                      30
135     aca acc tca ctc ccc tgg agg gcc gag ggg agg cct ggg gag gag ggg 264
136     Thr Thr Ser Leu Pro Trp Arg Ala Glu Gly Arg Pro Gly Glu Glu Gly
137         35                      40                      45
138     gcc tca gcc cag ctg ctg ggg ggc tgg cct gtc tcc tgc cca ggc gag 312
139     Ala Ser Ala Gln Leu Leu Gly Gly Trp Pro Val Ser Cys Pro Gly Glu
140         50                      55                      60
141     gag tgc tgt tcc gag tgg gac tgc atg tgt gtc cag cct gaa ttc cac 360
142     Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
143         65                      70                      75                      80
144     tgc gga gac cct tgc tgc acg acc tgc cgg cac cac cct tgt ccc cca 408

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/512,363

DATE: 03/20/2000  
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145      Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
146              85              90              95
147      ggc cag ggg gta cag tcc cag ggg aaa ttc agt ttt ggc ttc cag tgt      456
148      Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
149              100              105              110
150      atc gac tgt gcc tcg ggg acc ttc tcc ggg ggc cac gaa ggc cac tgc      504
151      Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
152              115              120              125
153      aaa cct tgg aca gac tgc acc cag ttc ggg ttt ctc act gtg ttc cct      552
154      Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
155              130              135              140
156      ggg aac aag acc cac aac gct gtg tgc gtc cca ggg tcc ccg ccg gca      600
157      Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
158      145              150              155              160
159      gag ccg ctt ggg tgg ctg acc gtc gtc ctc ctg gcc gtg gcc gcc tgc      648
160      Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
161              165              170              175
162      gtc ctc ctc ctg acc tcg gcc cag ctt gga ctg cac atc tgg cag ctg      696
163      Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
164              180              185              190
165      agg agt cag tgc atg tgg ccc cga gag acc cag ctg ctg ctg gag gtg      744
166      Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
167              195              200              205
168      ccg ccg tcg acc gaa gac gcc aga agc tgc cag ttc ccc gag gaa gag      792
169      Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
170              210              215              220
171      cgg ggc gag cga tcg gca gag gag aag ggg cgg ctg gga gac ctg tgg      840
172      Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
173      225              230              235              240
174      gtg tgagcctggc cgctcctccgg ggccaccgac cgcagccagc ccctccccag      893
175      Val
W--> 176
177      gagctcccca ggccgcaggg gctctgcgtt ctgctctggg ccggggccctg ctccccctggc 953
178      agcagaagtg ggtgcaggaa ggtggcagtg accagcgccc tggaccatgc agtt      1007
179      <210> SEQ ID NO 4
180      <211> LENGTH: 241
181      <212> TYPE: PRT
182      <213> ORGANISM: Homo sapiens
183      <400> SEQUENCE: 4
184      Met Ala Pro Gly Glu Arg Asp Ser Trp Ile Asn Pro Gly Pro Asp Ser
185      1              5              10              15
186      Gln Pro Gly Ala Leu Cys Ser Leu Glu Pro Thr Val Gly Gly Glu Arg
187      20              25              30
188      Thr Thr Ser Leu Pro Trp Arg Ala Glu Gly Arg Pro Gly Glu Glu Gly
189      35              40              45
190      Ala Ser Ala Gln Leu Leu Gly Gly Trp Pro Val Ser Cys Pro Gly Glu
191      50              55              60
192      Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
193      65              70              75              80
194      Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro

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**RAW SEQUENCE LISTING**  
**PATENT APPLICATION US/09/512,363**

 DATE: 03/20/2000  
 TIME: 15:41:40

Input Set: I512363.RAW

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195              85              90              95
196  Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
197              100              105              110
198  Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
199              115              120              125
200  Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
201              130              135              140
202  Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
203  145              150              155              160
204  Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
205              165              170              175
206  Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
207              180              185              190
208  Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
209              195              200              205
210  Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
211              210              215              220
212  Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
213  225              230              235              240
214  Val
215  <210> SEQ ID NO 5
216  <211> LENGTH: 1074
217  <212> TYPE: DNA
218  <213> ORGANISM: Homo sapiens
219  <220> FEATURE:
220  <221> NAME/KEY: CDS
221  <222> LOCATION: (1)..(720)
222  <220> FEATURE:
223  <221> NAME/KEY: sig_peptide
224  <222> LOCATION: (1)..(57)
225  <220> FEATURE:
226  <221> NAME/KEY: mat_peptide
227  <222> LOCATION: (58)..(720)
228  <400> SEQUENCE: 5
229  atg ggc gcg ttt cgg gcc ctg tgc ggc ctg gcg ctg ctg tgc gcg ctc 48
230  Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu
231              -15              -10              -5
232  agc ctg ggt cag cgc ccc acc ggg ggt ccc ggg tgc ggc cct ggg cgc 96
233  Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg
234              -1 1              5              10
235  ctc ctg ctt ggg acg gga acg gac gcg cgc tgc tgc cgg gtt cac acg 144
236  Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr
237              15              20              25
238  acg cgc tgc tgc cgc gat tac ccg gcc cag ctg ctg ggg ggc tgg cct 192
239  Thr Arg Cys Cys Arg Asp Tyr Pro Ala Gln Leu Leu Gly Gly Trp Pro
240              30              35              40              45
241  gtc tcc tgc cca ggc gag gag tgc tgt tcc gag tgg gac tgc atg tgt 240
242  Val Ser Cys Pro Gly Glu Glu Cys Cys Ser Glu Trp Asp Cys Met Cys
243              50              55              60
244  gtc cag cct gaa ttc cac tgc gga gac cct tgc tgc acg acc tgc cgg 288

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I512363.RAW

Line	? Error/Warning	Original Text
176	W Invalid/Missing Amino Acid Numbering	
384	W "N" or "Xaa" used: Feature required	cgattaaccc ggggcgaaga atngtggttt ccgagtng
385	W "N" or "Xaa" used: Feature required	gccttgaaat tccaattgcg gaagaaccct tngcttgc
386	W "N" or "Xaa" used: Feature required	acctttgttc ccccaaagcc naagggggta anaattcc
452	W "N" or "Xaa" used: Feature required	ggccgagggg aggcctgggg aggagggggc ctcagccc
453	W "N" or "Xaa" used: Feature required	ctcctgcccga ggcgaggant gctgttccga gtgggaat
454	W "N" or "Xaa" used: Feature required	ccattgcgga gaaccttgct gcacgaattg ccggcaac
455	W "N" or "Xaa" used: Feature required	ggtnacattc ccaggggaan ttcatttttg gnttccat
456	W "N" or "Xaa" used: Feature required	ttntccgggg gccanaaggc aatgcaaaac ttgganaa
457	W "N" or "Xaa" used: Feature required	ttccngggaa aagaccanaa gtttttggtc caggtccc

Input Set: I512363.RAW

## PREVIOUSLY ERRORED SEQUENCES-EDITED

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1  <210> 28
2  <211> 241
3  <212> PRT
4  <213> Homo sapiens
5  <400> 28
6      Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
7          1                      5              10              15
8      Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
9          20                      25              30
10     Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
11          35                      40              45
12     Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
13          50                      55              60
14     Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
15          65                      70              75              80
16     Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
17          85                      90              95
18     Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
19          100                     105              110
20     Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
21          115                     120              125
22     Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
23          130                     135              140
24     Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
25          145                     150              155              160
26     Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
27          165                     170              175
28     Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
29          180                     185              190
30     Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
31          195                     200              205
32     Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
33          210                     215              220
34     Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
35          225                     230              235              240
36     Val

```